

SEQUENCE LISTING

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<120> METHODS AND COMPOSITIONS RELATING TO THE PHARMACOGENETICS OF DIFFERENT GENE VARIANTS

<130> ARCD:405WO

<140> UNKNOWN
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<151> 2004-03-05

<160> 11

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Arg Thr Lys Arg Ser Ser Thr Thr Lys Leu Tyr Leu Ala Lys Gln Val
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Tyr	Ser	Arg	Gln	Trp	Cys	Val	Gln	Lys	Asn	Ser	Trp	Phe	Leu	Ser	Leu		
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cac atg ctg tgg tca agt gtt cta cag att gtc tta tct atc ttc ttc His Met Leu Trp Ser Ser Val Leu Gln Ile Val Leu Ser Ile Phe Phe 440	445	450	1399	
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gaa cat gat tcg gaa gcc aca gtc cga gat gtg aac ctg gac att atg Glu His Asp Ser Glu Ala Thr Val Arg Asp Val Asn Leu Asp Ile Met 650 655 660	2023
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		935	940	945
cta att aag aag gaa ttc ata gaa act gga aag gtg aag ttc tcc atc Leu Ile Lys Lys Glu Phe Ile Glu Thr Gly Lys Val Lys Phe Ser Ile				2935
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		970	975	980
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1030				1030
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 Leu His Thr Ile Met Asp Ser Asp Lys Val Met Val Leu Asp Asn Gly
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 Thr Lys Phe
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Leu His Val Tyr Lys Ser Arg Thr Lys Arg Ser Ser Thr Thr Lys Leu
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Tyr Leu Ala Lys Gln Val Phe Val Gly Phe Leu Leu Ile Leu Ala Ala
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Ile Glu Leu Ala Leu Val Leu Thr Glu Asp Ser Gly Gln Ala Thr Val
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Pro Ala Val Arg Tyr Thr Asn Pro Ser Leu Tyr Leu Gly Thr Trp Leu
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Leu Val Leu Leu Ile Gln Tyr Ser Arg Gln Trp Cys Val Gln Lys Asn
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Ser Trp Phe Leu Ser Leu Phe Trp Ile Leu Ser Ile Leu Cys Gly Thr
 130 135 140

Phe Gln Phe Gln Thr Leu Ile Arg Thr Leu Leu Gln Gly Asp Asn Ser
 145 150 155 160

Asn Leu Ala Tyr Ser Cys Leu Phe Phe Ile Ser Tyr Gly Phe Gln Ile
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Asn Pro Ser Ser Ile Ala Ser Phe Leu Ser Ser Ile Thr Tyr Ser Trp
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Asp Val Trp Glu Val Asp Glu Glu Met Lys Thr Lys Thr Leu Val Ser
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Val Pro Lys Ser Trp Leu Met Lys Ala Leu Phe Lys Thr Phe Tyr Met
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Val Leu Ser Ile Phe Phe Leu Trp Arg Glu Leu Gly Pro Ser Val Leu
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Ala Gly Val Gly Val Met Val Leu Val Ile Pro Ile Asn Ala Ile Leu
 465 470 475 480

Ser Thr Lys Ser Lys Thr Ile Gln Val Lys Asn Met Lys Asn Lys Asp
 485 490 495

Lys Arg Leu Lys Ile Met Asn Glu Ile Leu Ser Gly Ile Lys Ile Leu
 500 505 510

Lys Tyr Phe Ala Trp Glu Pro Ser Phe Ara Asp Gln Val Gln Asn Leu

515	520	525
Arg Lys Lys Glu Leu Lys Asn	Leu Leu Ala Phe Ser	Gln Leu Gln Cys
530	535	540
Val val Ile Phe Val Phe	Gln Leu Thr Pro Val	Leu Val Ser Val Val
545	550	555
Thr Phe Ser Val Tyr Val	Leu Val Asp Ser	Asn Asn Ile Leu Asp Ala
565	570	575
Gln Lys Ala Phe Thr Ser Ile	Thr Leu Phe Asn Ile	Leu Arg Phe Pro
580	585	590
Leu Ser Met Leu Pro Met Met	Ile Ser Ser Met	Leu Gln Ala Ser Val
595	600	605
Ser Thr Glu Arg Leu Glu Lys	Tyr Leu Gly Gly Asp	Asp Leu Asp Thr
610	615	620
Ser Ala Ile Arg His Asp Cys	Asn Phe Asp Lys	Ala Met Gln Phe Ser
625	630	635
Glu Ala Ser Phe Thr Trp	Glu His Asp Ser	Glu Ala Thr Val Arg Asp
645	650	655
Val Asn Leu Asp Ile Met Ala	Gly Gln Leu Val Ala Val	Ile Gly Pro
660	665	670
Val Gly Ser Gly Lys Ser Ser	Leu Ile Ser Ala Met	Leu Gly Glu Met
675	680	685
Glu Asn Val His Gly His	Ile Thr Ile Lys Gly Thr	Thr Ala Tyr Val
690	695	700
Pro Gln Gln Ser Trp Ile	Gln Asn Gly Thr Ile	Lys Asp Asn Ile Leu
705	710	715
Phe Gly Thr Glu Phe Asn Glu Lys Arg	Tyr Gln Gln Val	Leu Glu Ala
725	730	735
Cys Ala Leu Leu Pro Asp Leu Glu	Met Leu Pro Gly Gly Asp	Leu Ala
740	745	750
Glu Ile Gly Glu Lys Gly Ile	Asn Leu Ser Gly Gly	Gln Lys Gln Arg
755	760	765
Ile Ser Leu Ala Arg Ala Thr	Tyr Gln Asn Leu Asp	Ile Tyr Leu Leu
770	775	780
Asp Asp Pro Leu Ser Ala Val	Asp Ala His Val	Gly Lys His Ile Phe
785	790	795
Asn Lys Val Leu Gly Pro Asn	Gly Leu Leu Lys	Gly Lys Thr Arg Leu
805	810	815
Leu Val Thr His Ser Met His	Phe Leu Pro Gln Val Asp	Glu Ile Val
820	825	830
Val Leu Gly Asn Gly Thr Ile	Val Glu Lys Gly Ser	Tyr Ser Ala Leu
835	840	845
Leu Ala Lys Lys Gly Glu	Phe Ala Lys Asn Leu Lys	Thr Phe Leu Arg
850	855	860
His Thr Gly Pro Glu Glu	Glu Ala Thr Val His	Asp Gly Ser Glu Glu
865	870	875
Glu Asp Asp Asp Tyr Gly	Leu Ile Ser Ser Val	Glu Ile Pro Glu
885	890	895
Asp Ala Ala Ser Ile Thr Met	Arg Arg Glu Asn Ser	Phe Arg Arg Thr
900	905	910
Leu Ser Arg Ser Ser Arg	Ser Asn Gly Arg His	Leu Lys Ser Leu Arg
915	920	925
Asn Ser Leu Lys Thr Arg	Asn Val Asn Ser	Leu Lys Glu Asp Glu Glu
930	935	940
Leu Val Lys Gly Gln Lys	Leu Ile Lys Lys	Glu Phe Ile Glu Thr Gly
945	950	955
Lys Val Lys Phe Ser Ile	Tyr Leu Glu Tyr	Leu Gln Ala Ile Gly Leu
965	970	975
Phe Ser Ile Phe Phe Ile	Ile Leu Ala Phe Val	Met Asn Ser Val Ala
980	985	990
Phe Ile Gly Ser Asn Leu Trp	Leu Ser Ala Trp Thr	Ser Asp Ser Lys
995	1000	1005
Ile Phe Asn Ser Thr Asp Tyr	Pro Ala Ser Gln Arg	Asp Met Arg Val
1010	1015	1020

Gly Val Tyr Gly Ala Leu Gly Leu Ala Gln Gly Ile Phe Val Phe Ile
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 Ala His Phe Trp Ser Ala Phe Gly Phe Val His Ala Ser Asn Ile Leu
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 His Lys Gln Leu Leu Asn Asn Ile Leu Arg Ala Pro Met Arg Phe Phe
 1060 1065 1070
 Asp Thr Thr Pro Thr Gly Arg Ile Val Asn Arg Phe Ala Gly Asp Ile
 1075 1080 1085
 Ser Thr Val Asp Asp Thr Leu Pro Gln Ser Leu Arg Ser Trp Ile Thr
 1090 1095 1100
 Cys Phe Leu Gly Ile Ile Ser Thr Leu Val Met Ile Cys Met Ala Thr
 1105 1110 1115 1120
 Pro Val Phe Thr Ile Ile Val Ile Pro Leu Gly Ile Ile Tyr Val Ser
 1125 1130 1135
 Val Gln Met Phe Tyr Val Ser Thr Ser Arg Gln Leu Arg Arg Leu Asp
 1140 1145 1150
 Ser Val Thr Arg Ser Pro Ile Tyr Ser His Phe Ser Glu Thr Val Ser
 1155 1160 1165
 Gly Leu Pro Val Ile Arg Ala Phe Glu His Gln Gln Arg Phe Leu Lys
 1170 1175 1180
 His Asn Glu Val Arg Ile Asp Thr Asn Gln Lys Cys Val Phe Ser Trp
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 Ile Thr Ser Asn Arg Trp Leu Ala Ile Arg Leu Glu Leu Val Gly Asn
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 1220 1225 1230
 Leu Ser Gly Asp Thr Val Gly Phe Val Leu Ser Asn Ala Leu Asn Ile
 1235 1240 1245
 Thr Gln Thr Leu Asn Trp Leu Val Arg Met Thr Ser Glu Ile Glu Thr
 1250 1255 1260
 Asn Ile Val Ala Val Glu Arg Ile Thr Glu Tyr Thr Lys Val Glu Asn
 1265 1270 1275 1280
 Glu Ala Pro Trp Val Thr Asp Lys Arg Pro Pro Pro Asp Trp Pro Ser
 1285 1290 1295
 Lys Gly Lys Ile Gln Phe Asn Asn Tyr Gln Val Arg Tyr Arg Pro Glu
 1300 1305 1310
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 1315 1320 1325
 Lys Ile Gly Val Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Thr
 1330 1335 1340
 Asn Cys Leu Phe Arg Ile Leu Glu Ala Ala Gly Gly Gln Ile Ile Ile
 1345 1350 1355 1360
 Asp Gly Val Asp Ile Ala Ser Ile Gly Leu His Asp Leu Arg Glu Lys
 1365 1370 1375
 Leu Thr Ile Ile Pro Gln Asp Pro Ile Leu Phe Ser Gly Ser Leu Arg
 1380 1385 1390
 Met Asn Leu Asp Pro Phe Asn Asn Tyr Ser Asp Glu Glu Ile Trp Lys
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 Ala Leu Glu Leu Ala His Leu Lys Ser Phe Val Ala Ser Leu Gln Leu
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 Gly Leu Ser His Glu Val Thr Glu Ala Gly Gly Asn Leu Ser Ile Gly
 1425 1430 1435 1440
 Gln Arg Gln Leu Leu Cys Leu Gly Arg Ala Leu Leu Arg Lys Ser Lys
 1445 1450 1455
 Ile Leu Val Leu Asp Glu Ala Thr Ala Ala Val Asp Leu Glu Thr Asp
 1460 1465 1470
 Asn Leu Ile Gln Thr Thr Ile Gln Asn Glu Phe Ala His Cys Thr Val
 1475 1480 1485
 Ile Thr Ile Ala His Arg Leu His Thr Ile Met Asp Ser Asp Lys Val
 1490 1495 1500
 Met Val Leu Asp Asn Gly Lys Ile Ile Glu Cys Gly Ser Pro Glu Glu
 1505 1510 1515 1520
 Leu Leu Gln Ile Pro Gly Pro Phe Tyr Phe Met Ala Lys Glu Ala Gly

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1540	1545	

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<212> DNA
<213> Homo sapiens

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ggag 184

<210> 4
<211> 261
<212> DNA
<213> Human immunodeficiency virus type 1

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aattgcacaa gaccagcaa caatacaagg aaaagtatac atataggacc agggaaagca 120
tttatgcaa caggaagcat aataggagat ataagacaag cacattgtaa ccttagtaga 180
acacaatgga ataacacttt agaacagata gttaaaaaat taagagaaca attaaaaat 240
aaaacaatag ctttaagca c 261

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<212> DNA
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ttaatttctg gaaaagaagc ctaacttgtt cactacatag tcgtccttct tcctctctgg 180
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acctttgtgg actgacagct ttttacagtc acgtgacaca gtcaaacatt aacttgggt 420
atcgatttgtt ttttgcata tatatatata agtaggagag ggcgaacctc tggcaggagc 480
aaaggcgc 488

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<211> 490
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acctttgtgg actgacagct tttatagtc acgtgacaca gtcaaacatt aacttgggt 420
atcgatttgtt ttttgcata tatatatata taagtaggag agggcgaacc tctggcagga 480
gcaaaggcgc 490

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<211> 492
<212> DNA
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ttaattttg gaaaagaagc ctaacttggt cactacatag tcgtccttct tcctctctgg 180
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tgctgtgttc actcaagaat gtgatttgag tatgaaattc cagccagttc aactgttgg 300
gcctattaag aaacctaata aagctccacc ttcttatct ctgaaagtga actccctgct 360
acctttgtgg actgacagct tttatagtc acgtgacaca gtcaaacatt aacttgggt 420
atcgatttgtt tttgccata tatatatata tataagttagg agagggcgaa cctctggcag 480
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ttaattttg gaaaagaagc ctaacttggt cactacatag tcgtccttct tcctctctgg 180
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tgctgtgttc actcaagaat gtgatttgag tatgaaattc cagccagttc aactgttgg 300
gcctattaag aaacctaata aagctccacc ttcttatct ctgaaagtga actccctgct 360
acctttgtgg actgacagct tttatagtc acgtgacaca gtcaaacatt aacttgggt 420
atcgatttgtt tttgccata tatatatata tatataagta ggagagggcg aacctctggc 480
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<211> 2830
<212> DNA
<213> Homo sapiens

<220>
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<222> (135)..(2210)

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attctaaatc caggtgattt tttcaaactg agcatcaaca acaaaaacat ttgtatgata 120
tctatatttc aatc atg gac caa aat caa cat ttg aat aaa aca gca gag 170
Met Asp Gln Asn Gln His Leu Asn Lys Thr Ala Glu
1 5 10

gca caa cct tca gag aat aag aaa aca aga tac tgc aat gga ttg aag 218
Ala Gln Pro Ser Glu Asn Lys Lys Thr Arg Tyr Cys Asn Gly Leu Lys
15 20 25

atg ttc ttg gca gct ctg tca ctc agc ttt att gct aag aca cta ggt 266
Met Phe Leu Ala Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly
30 35 40

gca att att atg aaa agt tcc atc att cat ata gaa cgg aga ttt gag 314

Ala	Ile	Ile	Met	Lys	Ser	Ser	Ile	Ile	His	Ile	Glu	Arg	Arg	Phe	Glu		
45					50				55			60					
ata	tcc	tct	tct	ctt	ggt	ttt	att	gac	gga	agc	ttt	gaa	att	gga		362	
Ile	Ser	Ser	Ser	Leu	Val	Gly	Phe	Ile	Asp	Gly	Ser	Phe	Glu	Ile	Gly		
				65				70				75					
aat	ttg	ctt	gtg	att	gta	ttt	gtg	agt	tac	ttt	gga	tcc	aaa	cta	cat		410
Asn	Leu	Leu	Val	Ile	Val	Phe	Val	Ser	Tyr	Phe	Gly	Ser	Lys	Leu	His		
				80				85				90					
aga	cca	aag	tta	att	gga	atc	ggt	tgt	ttc	att	atg	gga	att	gga	ggt		458
Arg	Pro	Lys	Leu	Ile	Gly	Ile	Gly	Cys	Phe	Ile	Met	Gly	Ile	Gly	Gly		
				95				100				105					
gtt	ttg	act	gct	ttg	cca	cat	ttc	ttc	atg	gga	tat	tac	agg	tat	tct		506
Val	Leu	Thr	Ala	Leu	Pro	His	Phe	Phe	Met	Gly	Tyr	Tyr	Arg	Tyr	Ser		
				110			115				120						
aaa	gaa	act	aat	atc	gat	tca	tca	gaa	aat	tca	aca	tcg	acc	tta	tcc		554
Lys	Glu	Thr	Asn	Ile	Asp	Ser	Ser	Glu	Asn	Ser	Thr	Ser	Thr	Leu	Ser		
				125			130				135			140			
act	tgt	tta	att	aat	caa	att	tta	tca	ctc	aat	aga	gca	tca	cct	gag		602
Thr	Cys	Leu	Ile	Asn	Gln	Ile	Leu	Ser	Leu	Asn	Arg	Ala	Ser	Pro	Glu		
				145			150				155						
ata	gtg	gga	aaa	ggt	tgt	tta	aag	gaa	tct	ggg	tca	tac	atg	tgg	ata		650
Ile	Val	Gly	Lys	Gly	Cys	Leu	Lys	Glu	Ser	Gly	Ser	Tyr	Met	Trp	Ile		
				160			165				170						
tat	gtg	ttc	atg	ggt	aat	atg	ctt	cgt	gga	ata	ggg	gag	act	ccc	ata		698
Tyr	Val	Phe	Met	Gly	Asn	Met	Leu	Arg	Gly	Ile	Gly	Glu	Thr	Pro	Ile		
				175			180				185						
gta	cca	ttg	ggg	ctt	tct	tac	att	gat	gat	ttc	gct	aaa	gaa	gga	cat		746
Val	Pro	Leu	Gly	Leu	Ser	Tyr	Ile	Asp	Asp	Phe	Ala	Lys	Glu	Gly	His		
				190			195				200						
tct	tct	ttg	tat	tta	ggt	ata	ttg	aat	gca	ata	gca	atg	att	ggt	cca		794
Ser	Ser	Leu	Tyr	Leu	Gly	Ile	Leu	Asn	Ala	Ile	Ala	Met	Ile	Gly	Pro		
				205			210				215			220			
atc	att	ggc	ttt	acc	ctg	gga	tct	ctg	ttt	tct	aaa	atg	tac	gtg	gat		842
Ile	Ile	Gly	Phe	Thr	Leu	Gly	Ser	Leu	Phe	Ser	Lys	Met	Tyr	Val	Asp		
				225			230				235						
att	gga	tat	gta	gat	cta	agc	act	atc	agg	ata	act	cct	act	gat	tct		890
Ile	Gly	Tyr	Val	Asp	Leu	Ser	Thr	Ile	Arg	Ile	Thr	Pro	Thr	Asp	Ser		
				240			245				250						
cga	tgg	gtt	gga	gct	tgg	ttt	aat	ttc	ttt	gtg	tct	gga	cta	ttc		938	
Arg	Trp	Val	Gly	Ala	Trp	Trp	Leu	Asn	Phe	Leu	Val	Ser	Gly	Leu	Phe		
				255			260				265						
tcc	att	att	tct	tcc	ata	cca	ttc	ttt	ttc	ttg	ccc	caa	act	cca	aat		986
Ser	Ile	Ile	Ser	Ser	Ile	Pro	Phe	Phe	Phe	Leu	Pro	Gln	Thr	Pro	Asn		
				270			275				280						
aaa	cca	caa	aaa	gaa	aga	aaa	gct	tca	ctg	tct	ttg	cat	gtg	ctg	gaa		1034
Lys	Pro	Gln	Lys	Glu	Arg	Lys	Ala	Ser	Leu	Ser	Leu	His	Val	Leu	Glu		
				285			290				295			300			

aca aat gat gaa aag gat caa aca gct aat ttg acc aat caa gga aaa	1082
Thr Asn Asp Glu Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys	
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315	
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Asn Ile Thr Lys Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile	
320	325
330	
ctt act aat ccc ctg tat gtt atg ttt gtg ctt ttg acg ttg tta caa	1178
Leu Thr Asn Pro Leu Tyr Val Met Phe Val Leu Leu Thr Leu Leu Gln	
335	340
345	
gta agc agc tat att ggt gct ttt act tat gtc ttc aaa tac gta gag	1226
Val Ser Ser Tyr Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu	
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caa cag tat ggt cag cct tca tct aag gct aac atc tta ttg gga gtc	1274
Gln Gln Tyr Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val	
365	370
375	380
ata acc ata cct att ttt gca agt gga atg ttt tta gga gga tat atc	1322
Ile Thr Ile Pro Ile Phe Ala Ser Gly Met Phe Leu Gly Gly Tyr Ile	
385	390
395	
att aaa aaa ttc aaa ctg aac acc gtt gga att gcc aaa ttc tca tgt	1370
Ile Lys Lys Phe Lys Leu Asn Thr Val Gly Ile Ala Lys Phe Ser Cys	
400	405
410	
ttt act gct gtg atg tca ttg tcc ttt tac cta tta tat ttt ttc ata	1418
Phe Thr Ala Val Met Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile	
415	420
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ctc tgt gaa aac aaa tca gtt gcc gga cta acc atg acc tat gat gga	1466
Leu Cys Glu Asn Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly	
430	435
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aat aat cca gtg aca tct cat aga gat gta cca ctt tct tat tgc aac	1514
Asn Asn Pro Val Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn	
445	450
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tca gac tgc aat tgt gat gaa agt caa tgg gaa cca gtc tgt gga aac	1562
Ser Asp Cys Asn Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn	
465	470
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aat gga ata act tac atc tca ccc tgt cta gca ggt tgc aaa tct tca	1610
Asn Gly Ile Thr Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser	
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agt ggc aat aaa aag cct ata gtg ttt tac aac tgc agt tgt ttg gaa	1658
Ser Gly Asn Lys Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu	
495	500
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gta act ggt ctc cag aac aga aat tac tca gcc cat ttg ggt gaa tgc	1706
Val Thr Gly Leu Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys	
510	515
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cca aga gat gat gct tgt aca agg aaa ttt tac ttt ttt gtt gca ata	1754
Pro Arg Asp Asp Ala Cys Thr Arg Lys Phe Tyr Phe Phe Val Ala Ile	
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Gln Val Leu Asn Leu Phe Phe Ser Ala Leu Gly Gly Thr Ser His Val	
545	550
555	

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ctt gtt tta tat att ata tta att tat gcc atg aag aaa aaa tat caa Leu Val Leu Tyr Ile Ile Tyr Ala Met Lys Lys Lys Tyr Gln 640 645 650	2090
gag aaa gat atc aat gca tca gaa aat gga agt gtc atg gat gaa gca Glu Lys Asp Ile Asn Ala Ser Glu Asn Gly Ser Val Met Asp Glu Ala 655 660 665	2138
aac tta gaa tcc tta aat aaa aat cat ttt gtc cct tct gct ggg Asn Leu Glu Ser Leu Asn Lys Asn Lys His Phe Val Pro Ser Ala Gly 670 675 680	2186
gca gat agt gaa aca cat tgt taa ggggagaaaa aaagccactt ctgcttctgt Ala Asp Ser Glu Thr His Cys 685 690	2240
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<211> 3000
<212> DNA
<213> Homo sapiens

<220>
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<222> (2897) .. (2929)

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gcaccacgcc cggccaattt tttgtatTT tagtagagac agggttcac tgtggtctcg 360
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